

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a Mlo homolog polypeptide of at least 66 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38,
or a second nucleotide sequence comprising the complement of the first nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.
3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.
4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.
5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. A host cell comprising an isolated polynucleotide of Claim 1.
8. The host cell of Claim 7 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.
9. A virus comprising the isolated polynucleotide of Claim 1.
10. A polypeptide of at least 66 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.
11. A method of selecting an isolated polynucleotide that affects the level of expression of an Mlo homolog polypeptide in a plant cell, the method comprising the steps of:
 - (a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from an isolated polynucleotide of Claim 1;
 - (b) introducing the isolated polynucleotide into a plant cell; and
 - (c) measuring the level of a polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.

12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38.
13. A method of selecting an isolated polynucleotide that affects the level of expression of an Mlo homolog polypeptide in a plant cell, the method comprising the steps of:
- (a) constructing an isolated polynucleotide of Claim 1;
 - (b) introducing the isolated polynucleotide into a plant cell; and
 - (c) measuring the level of polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.
14. A method of obtaining a nucleic acid fragment encoding an Mlo homolog polypeptide comprising the steps of:
- (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 and the complement of such nucleotide sequences; and
 - (b) amplifying a nucleic acid sequence using the oligonucleotide primer.
15. A method of obtaining a nucleic acid fragment encoding an Mlo homolog polypeptide comprising the steps of:
- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 and the complement of such nucleotide sequences;
 - (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
 - (c) isolating the identified DNA clone; and
 - (d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.
16. A composition comprising the isolated polynucleotide of Claim 1.
17. A composition comprising the isolated polypeptide of Claim 10.
18. An isolated polynucleotide comprising the nucleotide sequence having at least one of 30 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, and the complement of such sequences.
19. An expression cassette comprising an isolated polynucleotide of Claim 1 operably linked to a promoter.
20. A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the chimeric gene of Claim 5 or an expression cassette of Claim 19; and

(b) growing the transformed host cell under conditions which allow expression of the polynucleotide in an amount sufficient to complement a null mutant to provide a positive selection means.

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21. The method of Claim 20 wherein the host cell is a plant cell.

22. The method of Claim 21 wherein the plant cell is a monocot.

23. The method of Claim 21 wherein the plant cell is a dicot.

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